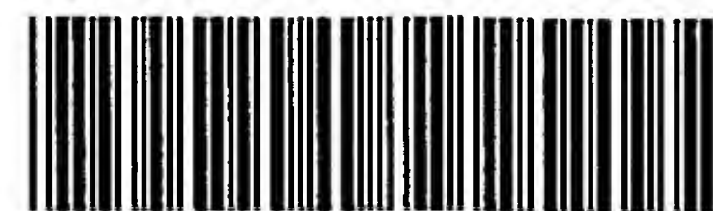# <u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/567, 749 A

Source: _____ IFWO,

Date Processed by STIC: _____ 12/28/2006

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IFWO

RAW SEQUENCE LISTING   DATE: 12/28/2006
PATENT APPLICATION: US/10/567,749A   TIME: 09:27:00

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 3 <110> APPLICANT: Kruse, Daniela
 4         Hertmann, Thomas
 5         Thierbach, Georg
 6         Rieping, Mechthild
 9 <120> TITLE OF INVENTION: A Process for Preparing L-Threonione
11 <130> FILE REFERENCE: 7601/88025
13 <140> CURRENT APPLICATION NUMBER: 10/567749A
14 <141> CURRENT FILING DATE: 2006-02-10
16 <160> NUMBER OF SEQ ID NOS: 10
18 <170> SOFTWARE: PatentIn version 3.4
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21 <211> LENGTH: 993
22 <212> TYPE: DNA
23 <213> ORGANISM: Escherichia coli
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28 <223> OTHER INFORMATION: rpos gene
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33 1               5                   10                  15
35 ttt gat gag aac gga gtt gag gtt ttt gac gaa aag gcc tta gta gaa     96
36 Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu
37                 20                  25                  30
39 cag gaa ccc agt gat aac gat ttg gcc gaa gag gaa ctg tta tcg cag    144
40 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln
41                 35                  40                  45
43 gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag    192
44 Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
45         50                  55                  60
47 att ggt tat tca cca ctg tta acg gcc gaa gaa gaa gtt tat ttt gcg    240
48 Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala
49 65                  70                  75                  80
51 cgt cgc gca ctg cgt gga gat gtc gcc tct cgc cgc cgg atg atc gag    288
52 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
53                 85                  90                  95
55 agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt    336
56 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
57                 100                 105                 110
59 ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc    384
60 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
61         115                 120                 125
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63 cgc gcg gta gag aag ttt gac ccg gaa cgt ggt ttc cgc ttc tca aca    432
64 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
65     130             135             140
67 tac gca acc tgg tgg att cgc cag acg att gaa cgg gcg att atg aac    480
68 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
69 145                 150             155                 160
71 caa acc cgt act att cgt ttg ccg att cac atc gta aag gag ctg aac    528
72 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
73                 165             170             175
75 gtt tac ctg cga acc gca cgt gag ttg tcc cat aag ctg gac cat gaa    576
76 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
77             180             185             190
79 cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac    624
80 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
81             195             200             205
83 gtc agc cgt atg ctt cgt ctt aac gag cgc att acc tcg gta gac acc    672
84 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
85     210             215             220
87 ccg ctg ggt ggt gat tcc gaa aaa gcg ttg ctg gac atc ctg gcc gat    720
88 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
89 225             230             235             240
91 gaa aaa gag aac ggt ccg gaa gat acc acg caa gat gac gat atg aag    768
92 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
93                 245             250             255
95 cag agc atc gtc aaa tgg ctg ttc gag ctg aac gcc aaa cag cgt gaa    816
96 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
97             260             265             270
99 gtg ctg gca cgt cga ttc ggt ttg ctg ggg tac gaa gcg gca aca ctg    864
100 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
101             275             280             285
103 gaa gat gta ggt cgt gaa att ggc ctc acc cgt gaa cgt gtt cgc cag   912
104 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
105     290             295             300
107 att cag gtt gaa ggc ctg cgc cgt ttg cgc gaa atc ctg caa acg cag   960
108 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
109 305             310             315             320
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117 <211> LENGTH: 330
118 <212> TYPE: PRT
119 <213> ORGANISM: Escherichia coli
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126             20              25              30
128 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln
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129          35                   40                   45
131 Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
132     50                   55                   60
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135 65                   70                   75                   80
137 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
138             85                   90                   95
140 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
141             100                  105                  110
143 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
144         115                  120                  125
146 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
147     130                  135                  140
149 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
150 145                  150                  155                  160
152 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
153             165                  170                  175
155 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
156         180                  185                  190
158 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
159     195                  200                  205
161 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
162     210                  215                  220
164 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
165 225                  230                  235                  240
167 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
168             245                  250                  255
170 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
171         260                  265                  270
173 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
174     275                  280                  285
176 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
177     290                  295                  300
179 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
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193 <222> LOCATION: (1)..(990)
194 <223> OTHER INFORMATION: rpoS allele
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197 <221> NAME/KEY: misc_feature
198 <222> LOCATION: (97)..(99)
199 <223> OTHER INFORMATION: amber codon
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RAW SEQUENCE LISTING   DATE: 12/28/2006
PATENT APPLICATION: US/10/567,749A   TIME: 09:27:00

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Output Set: N:\CRF4\12282006\J567749A.raw

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206 gccgaagagg aactgttatc gcagggagcc acacagcgtg tgttggacgc gactcagctt  180
208 taccttggtg agattggtta ttcaccactg ttaacggccg aagaagaagt ttattttgcg  240
210 cgtcgcgcac tgcgtggaga tgtcgcctct cgccgccgga tgatcgagag taacttgcgt  300
212 ctggtggtaa aaattgcccg ccgttatggc aatcgtggtc tggcgttgct ggaccttatc  360
214 gaagagggca acctggggct gatccgcgcg gtagagaagt ttgacccgga acgtggtttc  420
216 cgcttctcaa catacgcaac ctggtggatt cgccagacga ttgaacgggc gattatgaac  480
218 caaacccgta ctattcgttt gccgattcac atcgtaaagg agctgaacgt ttacctgcga  540
220 accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaga gatcgcagag  600
222 caactggata agccagttga tgacgtcagc cgtatgcttc gtcttaacga gcgcattacc  660
224 tcggtagaca ccccgctggg tggtgattcc gaaaaagcgt tgctggacat cctggccgat  720
226 gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc  780
228 aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg  840
230 ctggggtacg aagcggcaac actggaagat gtaggtcgtg aaattggcct cacccgtgaa  900
232 cgtgttcgcc agattcaggt tgaaggcctg cgccgtttgc gcgaaatcct gcaaacgcag  960
234 gggctgaata tcgaagcgct gttccgcgag taa                                993
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238 <211> LENGTH: 75
239 <212> TYPE: DNA
240 <213> ORGANISM: Escherichia coli
242 <220> FEATURE:
243 <221> NAME/KEY: tRNA
244 <222> LOCATION: (1)..(75)
245 <223> OTHER INFORMATION: supE allele
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255 <211> LENGTH: 1545
256 <212> TYPE: DNA
257 <213> ORGANISM: Escherichia coli
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262 <223> OTHER INFORMATION: ilvA-Gen
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267 1               5                   10                  15
269 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg   96
270 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
271             20                  25                  30
273 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att  144
274 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
275         35                  40                  45
277 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc  192
278 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
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279      50                    55                    60
281 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac    240
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283 65                    70                    75                    80
285 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt    288
286 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
287                    85                    90                    95
289 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc    336
290 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
291                    100                   105                   110
293 acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg    384
294 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
295                    115                   120                   125
297 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa    432
298 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
299          130                   135                   140
301 ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg    480
302 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
303 145                   150                   155                   160
305 atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag    528
306 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
307                    165                   170                   175
309 gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg    576
310 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
311          180                   185                   190
313 gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa    624
314 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
315          195                   200                   205
317 gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg    672
318 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
319          210                   215                   220
321 gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa    720
322 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
323 225                   230                   235                   240
325 ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag    768
326 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
327          245                   250                   255
329 gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg    816
330 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
331          260                   265                   270
333 gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg gaa ccc tct    864
334 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser
335          275                   280                   285
337 ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac    912
338 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
339          290                   295                   300
341 att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac    960
342 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
343 305                   310                   315                   320
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VERIFICATION SUMMARY   DATE: 12/28/2006
PATENT APPLICATION: US/10/567,749A   TIME: 09:27:01

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